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RAW SEQUENCE LISTING

DATE: 04/11/2002

PATENT APPLICATION: US/10/031,547

TIME: 09:22:53

Input Set : N:\Crf3\04102002\J031547.raw

Output Set: N:\CRF3\04112002\J031547.raw

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1 <110> APPLICANT: Rupert, PFALLER
2 <120> TITLE OF INVENTION: pyrF GENE AND ITS USE
3 <130> FILE REFERENCE: PFALLER-1 US PCT
4 <140> CURRENT APPLICATION NUMBER: US/10/031,547
5 <141> CURRENT FILING DATE: 2002-01-18
6 <150> PRIOR APPLICATION NUMBER: PCT/EP00/06091
7 <151> PRIOR FILING DATE: 2000-06-29
8 <160> NUMBER OF SEQ ID NOS: 7
9 <170> SOFTWARE: PatentIn version 3.1
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 3448
13 <212> TYPE: DNA
14 <213> ORGANISM: Trametes versicolor
15 <220> FEATURE:
16 <221> NAME/KEY: gene
17 <222> LOCATION: (1133)..(1877)
18 <223> OTHER INFORMATION:
19 <221> NAME/KEY: promoter
20 <222> LOCATION: (1)..(1132)
21 <223> OTHER INFORMATION:
W--> 22 <221> 3'UTR
23 <222> LOCATION: (1878)..(3448)
24 <223> OTHER INFORMATION:
W--> 25 <221> Intron
26 <222> LOCATION: (1226)..(1286)
27 <223> OTHER INFORMATION:
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31      gaggcgagag tatagagata tccctaggag tgtgacgtca tcggacgagt taccctcgcg      180
32      ggtatgttgt gtactgtcca ccttctccgg gtcagacggg tgtgatgtac tgcgtccggg      240
33      ttggagcgtc aggaaaagcg cagacaggct gaagagtccc attccgcgcg agaagggtgtg      300
34      cgagggggaa agtgccagt tagcagttag gcgtgcctac gatatgagac ggacatggtc      360
35      agtatctatg cccggtcaag gtcgccgcac agacctcact gtaacctcat ggcaatgtcg      420
36      cggatgcaca aagcaggtag agatgttcaa atggggcacg gaggcgggtcg tccggagcgc      480
37      tctccctcgg ctctttgcaa ggcagctggc ggatgtttgg tcagttgagg tactgcatcc      540
38      cttgcaatag cgaaaacagc tcaccagacg tgagtatatg ctgtatacgg gagaaggaag      600
39      cggaacaccg tgagtggaag agatgaagtg gttatgaata catcccgggtg gaggttgagt      660
40      ctaacagcgt cggatctcgc tgcgttccgg agcagaggcc cggtaacgagc gccgggtgtct      720
41      gctcgtgttc cggcacgccg tatgctcgta aatcaccttt agaaaacttg aataagttag      780
42      agaagatacg aaacgtcagt ctgcacctat ggagatatgt aaaaatcgca aaaacatagc      840
43      gttgacgcta taaaaagaa aaggacaaaa tgaccaccgc aggggtcgaa cctgcaatct      900
44      cctgatccct aggtttgaag gttcatcacc tcaattcgta gtcagacgcg atgccatttc      960

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45 gccaggcggc cgtagaaac gaaactacta cgtttaaacc cgggtataac acagcctagt 1020
46 attccgtgcg ggccgcgcgc cgcataagct tgttttcgtg aactgtcttc cccctcctgc 1080
47 atctcgattc tcgacctcca tcgccgcgac gatcccttcc tcccactca ccatgtcgct 1140
48 cgaaaaatac cagacagagc tcacgagca cggcatgacc gccggtgcgc tcaagttcgg 1200
49 gaccttcacc ctcaaactcg gccggtccgt cccctcccta ggtgcgcgc cgtctctccc 1260
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59 aggagcacgg ccgacggag gagcttgca agatgcaaga gtactgggag cagtacggcg 1860
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61 tacatcgatc catccactaa acccatgcag atgaagaccc actgtacaat ttctcggtac 1980
62 ctgtcacgtt gaacgcaaag agccgaagat gtgagagtac acatgccatt catcccgata 2040
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64 tccatgggca ctgagttatg atgaactaac cgctatcacc aaaaacaccg ctcttattcg 2160
65 cccaaccgac gaccgaacc ccagttatat cctcccacac cgctcgcagc agcagcagca 2220
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75 ttggaatttc gactagtttc aagtgtacgg tccctcagat catcatgtat tgcaacagtg 2820
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79 ctgacttacc tttcatccaa ctacagagac agaaacccac ctcaaacttc tgcgtaacga 3060
80 actccttcac aaagacgacc ttgtatatg gcaagatttg caggagcact ggcaagggtga 3120
81 cggcgagaga ggaggcgcat agaaaccgag tgactggagg gattttgcga atctcatcca 3180
82 tgaaagacat cttgaggaga ctggagggtga gttagagcag agaagtagag caggcagagc 3240
83 agagacgacg gcagaatgtg gggaagaaca agcaggagga ggagtagagt gattttgaag 3300
84 taatgaaaag tggcgcaacc taatgcaaag tgtatgaggg acatccgtgg acataaagta 3360
85 ttccgcacct cgggcaagac attcaatctc agtaatgcac ttcactttcg gaggttcaact 3420
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88 <210> SEQ ID NO: 2

89 <211> LENGTH: 684

90 <212> TYPE: DNA

91 <213> ORGANISM: Trametes versicolor

92 <220> FEATURE:

93 <221> NAME/KEY: CDS

94 <222> LOCATION: (1)..(684)

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95 <223> OTHER INFORMATION:

96 <400> SEQUENCE: 2

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99      1          5          10          15
100     gcc ggt gcg ctc aag ttc ggg acc ttc acc ctc aaa tca ggc cgg acc      96
101     Ala Gly Ala Leu Lys Phe Gly Thr Phe Thr Leu Lys Ser Gly Arg Thr
102           20          25          30
103     tcg ccc tac ttc ttc aac gcc ggc ctg ctc gcg tcc ggg ccc gtg ctc      144
104     Ser Pro Tyr Phe Phe Asn Ala Gly Leu Leu Ala Ser Gly Pro Val Leu
105           35          40          45
106     gac acg ctg tgc tcc gcg tac gcc gcg acg atc gcg cgc gcg ctc aag      192
107     Asp Thr Leu Cys Ser Ala Tyr Ala Ala Thr Ile Ala Arg Ala Leu Lys
108           50          55          60
109     gcg tcg ccc ggg ctg ccc gcg ttc gac gtg ctc ttc ggg ccc gcg tac      240
110     Ala Ser Pro Gly Leu Pro Ala Phe Asp Val Leu Phe Gly Pro Ala Tyr
111     65          70          75          80
112     aag ggc atc ccg ttc gcg gcg ggg acc gcg ctg ctg ctg cac cgc gac      288
113     Lys Gly Ile Pro Phe Ala Ala Gly Thr Ala Leu Leu Leu His Arg Asp
114           85          90          95
115     cac ggc atc acc gtc ggg ttc gcg tac gac cgc aag gag gcg aag gat      336
116     His Gly Ile Thr Val Gly Phe Ala Tyr Asp Arg Lys Glu Ala Lys Asp
117           100         105         110
118     cat ggg gag ggc ggg ata ctt gtg ggc gcg ccg gtg agg ggc aag cgc      384
119     His Gly Glu Gly Gly Ile Leu Val Gly Ala Pro Val Arg Gly Lys Arg
120           115         120         125
121     gtg ctg gtg ctg gac gac gtc gcg acg gcg ggc acg gcg atc cgc cag      432
122     Val Leu Val Leu Asp Asp Val Ala Thr Ala Gly Thr Ala Ile Arg Gln
123           130         135         140
124     gcg att gag act gtg acg aag gag ggg ggc gag gtc gtt ggc gcg gtg      480
125     Ala Ile Glu Thr Val Thr Lys Glu Gly Gly Glu Val Val Gly Ala Val
126     145         150         155         160
127     ttg atg ctc gat cgg cag gag gtg ggc aag gag ggg aag agc acg ctt      528
128     Leu Met Leu Asp Arg Gln Glu Val Gly Lys Glu Gly Lys Ser Thr Leu
129           165         170         175
130     gcg gag gtg gag gcg ctg ttg ggc ggg aag gga cgt gtg ccg acg atc      576
131     Ala Glu Val Glu Ala Leu Leu Gly Gly Lys Gly Arg Val Pro Thr Ile
132           180         185         190
133     ctg agg atg aag gac ctc atg aag tgg ttg cag gag cac ggc cgg acg      624
134     Leu Arg Met Lys Asp Leu Met Lys Trp Leu Gln Glu His Gly Arg Thr
135           195         200         205
136     gag gag ctt gcg aag atg caa gag tac tgg gag cag tac ggc gcg aag      672
137     Glu Glu Leu Ala Lys Met Gln Glu Tyr Trp Glu Gln Tyr Gly Ala Lys
138           210         215         220
139     gaa agc gaa tga      684
140     Glu Ser Glu
141     225
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 227

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145 <212> TYPE: PRT
146 <213> ORGANISM: Trametes versicolor
147 <400> SEQUENCE: 3
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149 1 5 10 15
150 Ala Gly Ala Leu Lys Phe Gly Thr Phe Thr Leu Lys Ser Gly Arg Thr
151 20 25 30
152 Ser Pro Tyr Phe Phe Asn Ala Gly Leu Leu Ala Ser Gly Pro Val Leu
153 35 40 45
154 Asp Thr Leu Cys Ser Ala Tyr Ala Ala Thr Ile Ala Arg Ala Leu Lys
155 50 55 60
156 Ala Ser Pro Gly Leu Pro Ala Phe Asp Val Leu Phe Gly Pro Ala Tyr
157 65 70 75 80
158 Lys Gly Ile Pro Phe Ala Ala Gly Thr Ala Leu Leu Leu His Arg Asp
159 85 90 95
160 His Gly Ile Thr Val Gly Phe Ala Tyr Asp Arg Lys Glu Ala Lys Asp
161 100 105 110
162 His Gly Glu Gly Gly Ile Leu Val Gly Ala Pro Val Arg Gly Lys Arg
163 115 120 125
164 Val Leu Val Leu Asp Asp Val Ala Thr Ala Gly Thr Ala Ile Arg Gln
165 130 135 140
166 Ala Ile Glu Thr Val Thr Lys Glu Gly Gly Glu Val Val Gly Ala Val
167 145 150 155 160
168 Leu Met Leu Asp Arg Gln Glu Val Gly Lys Glu Gly Lys Ser Thr Leu
169 165 170 175
170 Ala Glu Val Glu Ala Leu Leu Gly Gly Lys Gly Arg Val Pro Thr Ile
171 180 185 190
172 Leu Arg Met Lys Asp Leu Met Lys Trp Leu Gln Glu His Gly Arg Thr
173 195 200 205
174 Glu Glu Leu Ala Lys Met Gln Glu Tyr Trp Glu Gln Tyr Gly Ala Lys
175 210 215 220
176 Glu Ser Glu
177 225
179 <210> SEQ ID NO: 4
180 <211> LENGTH: 26
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Description of Artificial Sequence: PrimerA
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186 <222> LOCATION: (1)..(26)
187 <223> OTHER INFORMATION: n = i
W--> 188 <221> misc_feature
189 <222> LOCATION: (6)..(6)
190 <223> OTHER INFORMATION: n = i
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192 <222> LOCATION: (9)..(9)
193 <223> OTHER INFORMATION: n = i
W--> 194 <221> misc_feature

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195 <222> LOCATION: (12)..(12)
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198 <222> LOCATION: (21)..(21)
199 <223> OTHER INFORMATION: n = i
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W--> 201      ttyggncng cntayaargg nathcc                26
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204 <211> LENGTH: 23
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: PrimerB
W--> 209 <221> NAME/KEY: primer_bind
210 <222> LOCATION: (1)..(23)
211 <223> OTHER INFORMATION: n = i
W--> 212 <221> misc_feature
213 <222> LOCATION: (3)..(3)
214 <223> OTHER INFORMATION: n = i
W--> 215 <221> misc_feature
216 <222> LOCATION: (6)..(6)
217 <223> OTHER INFORMATION: n = i
W--> 218 <221> misc_feature
219 <222> LOCATION: (12)..(12)
220 <223> OTHER INFORMATION: n = i
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224 <210> SEQ ID NO: 6
225 <211> LENGTH: 35
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: PyF-1
W--> 230 <221> NAME/KEY: misc_feature
231 <222> LOCATION: (1)..(35)
232 <223> OTHER INFORMATION:
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234      ctagacatgt cgctcgaaaa ataccagaca gagct        35
236 <210> SEQ ID NO: 7
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: PyF-2
W--> 242 <221> NAME/KEY: misc_feature
243 <222> LOCATION: (1)..(35)
244 <223> OTHER INFORMATION:
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